AMENDMENTS TO THE SPECIFICATION

Please make the following amendments to the specification.

Please replace paragraphs 0201-0202 with the following paragraphs:

The PCR-product hybridization validation methodology used is briefly described as follows. In order to validate the expression of predicted novel GAM genes, and assuming that these novel genes are probably expressed at low concentrations, a PCR product cloning approach was set up through the following strategy: two types of cDNA libraries designated "One tailed"and "Ligation" were prepared from frozen HeLa S100 extract (4c Biotech, Belgium) size fractionated RNA. Essentially, Total S100 RNA was prepared through an SDS_Proteinase K incubation followed by an acid Phenol-Chloroform purification and Isopropanol precipitation. Alternatively, total HeLa RNA was also used as starting material for these libraries._Fractionation was done by loading up to 500µg per YM100 Amicon Microcon column (Millipore) followed by a 500g centrifugation for 40 minutes at 4ºC. Flowthrough "YM100" RNA consisting of about ¼ of the total RNA was used for library preparation or fractionated further by loading onto a YM30 Amicon Microcon column (Millipore) followed by a 13,500g centrifugation for 25 minutes at 4ºC. Flowthrough "YM30" was used for library preparation as is and consists of less than 0.5% of total RNA. For the both the "ligation"_and the "One-tailed"libraries RNA was ~~dephosphorilated~~ dephosphorylated and ligated to an RNA (lowercase)-DNA (UPPERCASE) hybrid 5"-~~phosphorilated~~ phosphorylated, 3" idT blocked 3"-adapter (5"-P-uuuAACCGCATTCTC-idT-3" (SEQ ID NO: 20201) Dharmacon # P-002045-01-05) (as elaborated in Elbashir et al 2001) resulting in ligation only of RNase III type cleavage products. 3"-Ligated RNA was excised and purified from a half 6%, half 13% polyacrylamide gel to remove excess adapter with a Nanosep 0.2µM centrifugal device (Pall) according to instructions, and precipitated with glycogen and 3 volumes of Ethanol. Pellet was resuspended in a minimal volume of water. For the "ligation" library a DNA (UPPERCASE)-RNA (lowercase) hybrid 5"-adapter (5"-TACTAATACGACTCACTaaa-3" (SEQ ID NO: 20202) Dharmacon # P-002046-01-05) was ligated to the 3"-adapted RNA, reverse transcribed with "EcoRI-RT": (5"-GACTAGCTGGAATTCAAGGATGCGGTTAAA-3" (SEQ ID NO: 20203)), PCR amplified with two external primers essentially as in Elbashir et al 2001 except that primers were "EcoRI-RT"and "PstI Fwd"___(5"-CAGCCAACGCTGCAGATACGACTCACT

AAA-3" (SEQ ID NO: 20204)). This PCR product was used as a template for a second round of PCR with one hemispecific and one external primer or with two hemispecific primers.

For the "One tailed" library the 3"-Adapted RNA was annealed to 20pmol primer "EcoRI RT" by heating to 70ºC and cooling 0.1ºC/sec to 30ºC and then reverse transcribed with Superscript II RT (According to instructions, Invitrogen) in a 20µl volume for 10 alternating 5 minute cycles of 37ºC and 45ºC. Subsequently, RNA was digested with 1µl 2M NaOH, 2mM EDTA at 65ºC for 10 minutes. cDNA was loaded on a polyacrylamide gel, excised and gel-purified from excess primer as above (invisible, judged by primer run alongside) and resuspended in 13µl of water. Purified cDNA was then oligo-dC tailed with 400U of recombinant terminal transferase (Roche molecular biochemicals), 1µl 100µM dCTP, 1µl 15mM CoCl2, and 4µl reaction buffer, to a final volume of 20µl for 15 minutes at 37ºC. Reaction was stopped with 2µl 0.2M EDTA and 15µl 3M NaOAc pH 5.2. Volume was adjusted to 150µl with water, Phenol : Bromochloropropane 10:1 extracted and subsequently precipitated with glycogen and 3 volumes of Ethanol. C-tailed cDNA was used as a template for PCR with the external primers "T3-PstBsg(G/I)18" (5"-AATTAACCCTCACTA AAGGCTGCAGGTGCAGGIGGGIIGGGIIGGGIIGN-3" (SEQ ID NO: 20205) where I stands for Inosine and N for any of the 4 possible deoxynucleotides), and with "EcoRI Nested" (5"-GGAATTCAAGGATGCGGTTA-3" (SEQ ID NO: 20206)). This PCR product was used as a template for a second round of PCR with one hemispecific and one external primer or with two hemispecific primers. Hemispecific primers were constructed for each predicted GAM by an in-house program designed to choose about half of the 5" or 3" sequence of the GAM corresponding to a ~~TMº~~ TM of about 30º-34ºC constrained by an optimized 3" clamp, appended to the cloning adapter sequence (for "One-tailed"libraries 5"-GGNNGGGNNG (SEQ ID NO: 20207) on the 5" end of the GAM, or 5"-TTTAACCGCATC-3" (SEQ ID NO: 20208) on the 3" end of the GAM. For "Ligation" libraries the same 3" adapter and 5"-CGACTCACTAAA (SEQ ID NO: 20209) on the 5" end). Consequently, a fully complementary primer of a ~~TMº~~ TM higher than 60ºC was created covering only one half of the GAM sequence permitting the unbiased elucidation by sequencing of the other half.

Please replace 0206 with the following paragraph:

Reference is now made to Fig. 23B, which is a schematic representation of secondary folding of each of the MIRs and GAMS of GR GR12731 MIR24 (SEQ ID NO: 20198), MIR23

(SEQ ID NO: 20192), GAM22 (SEQ ID NO: 20193) and GAM116 (SEQ ID NO: 20194), and of the negative control non-GAM hairpins, herein designated N2 (SEQ ID NO: 20190), N3 (SEQ ID NO: 20191), N116 (SEQ ID NO: 20216), N4 (SEQ ID NO: 20195), N6 (SEQ ID NO: 20197) and N7 (SEQ ID NO: 20199). N0 (SEQ ID NO: 20196) is a non-hairpin control, of a similar length to that of known MIR PRECURSOR hairpins. It is appreciated that the negative controls are situated adjacent to and in between real MIR genes and GAM predicted oligonucleotide and demonstrates similar secondary folding patterns to that of known MIRs and GAMS.

Please replace paragraph 0211 with the following paragraph:

Reference is now made to Fig. 24A which is an annotated sequence of an EST comprising a novel gene detected by the gene detection system of the present invention. Fig. 24A shows the nucleotide sequence of a known human non-protein coding EST (Expressed Sequence Tag), identified as EST72223 (SEQ ID NO: 20200). The EST72223 clone obtained from TIGR database (Kirkness and Kerlavage, 1997) was sequenced to yield the above 705bp transcript with a polyadenyl tail. It is appreciated that the sequence of this EST comprises sequences of one known miRNA gene, identified as MIR98, and of one novel GAM gene, referred to here as GAM25, detected by the bioinformatic gene detection system of the present invention and described hereinabove with reference to Fig. 9.

Please replace paragraph 0220 with the following paragraph:

Transcript products were 705nt (EST72223), 102nt (MIR98 precursor), 125nt (GAM25 precursor) long. EST72223 was PCR amplified with T7-EST 72223 forward primer: 5"-TAATACGACTCACTATAGGCCCTTATTAGAGGATTCTG CT-3" (SEQ ID NO: 20210) and T3-EST72223 reverse primer: 5"-AATTAACCCTCACTAAAGGTTTTTTTTTCCTGAGACAG AGT-3" (SEQ ID NO: 20211). MIR98 was PCR amplified using EST72223 as a template with T7MIR98 forward primer: 5-"TAATACGACTCACTATAGGGTGAGGTAGTAAGTTGTA TTGTT-3" (SEQ ID NO: 20212) and T3MIR98 reverse primer: 5"-AATTAACCCTCACTAAAGGGAAAGTAGTAAGTTGTAT AGTT-3" (SEQ ID NO: 20213). GAM25 was PCR amplified using EST72223 as a template with GAM25 forward primer: 5"-GAGGCAGGAGAATTGCTTGA-3" (SEQ ID NO: 20214) and T3-EST72223 reverse primer: 5"-AATTAACCCTCACTAAAGG CCTGAGACAGAGTCTTGCTC-3" (SEQ ID NO. 20215).